/646

CRF Errors Corrected by th STIC System Branch

Serial Number: 09/039,927

CRF Processing Date: 8/6/99
Edited by: ___
Verified by: ___ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: ~~ENTERED~~
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

> This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

```
 1                              SEQUENCE LISTING
 2                                                           Does Not Comply
 3     (1)     General Information:                    Corrected Diskette Needed
 4
 5         (i) APPLICANT: Lester, Henry A.
 6                        Davidson, Norman
 7                        Kofuji, Paulo
 8
 9        (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
10              MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
11
12       (iii) NUMBER OF SEQUENCES: 2
13
14        (iv) CORRESPONDENCE ADDRESS:
15             (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
16             (B) STREET: Four Embarcadero Center, Suite 3400
17             (C) CITY: San Francisco
18             (D) STATE: California
19             (E) COUNTRY: United States
20             (F) ZIP: 94111-4187
21
22         (v) COMPUTER READABLE FORM:
23             (A) MEDIUM TYPE: Floppy disk
24             (B) COMPUTER: IBM PC compatible
25             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28        (vi) CURRENT APPLICATION DATA:
29             (A) APPLICATION NUMBER: US 09/039,927
30             (B) FILING DATE: 16-MAR-1998
31             (C) CLASSIFICATION:
32
33       (vii) PRIOR APPLICATION DATA:
34             (A) APPLICATION NUMBER: US 08/066,371
35             (B) FILING DATE: 21-MAR-1993
36
37       (vii) PRIOR APPLICATION DATA:
38             (A) APPLICATION NUMBER: US 08/614,801
39             (B) FILING DATE: 07-MAR-1996
40
41      (viii) ATTORNEY/AGENT INFORMATION:
42             (A) NAME: Trecartin, Richard F.
43             (B) REGISTRATION NUMBER: 31,801
44             (C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
45
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,927*

INPUT SET: S32821.raw

```
46        (ix) TELECOMMUNICATION INFORMATION:
47             (A) TELEPHONE: (415) 781-1989
48             (B) TELEFAX: (415) 398-3249
49             (C) TELEX: 910 277299
50
```

ERRORED SEQUENCES FOLLOW:

```
51        (2) INFORMATION FOR SEQ ID NO:1:
52
53             (i) SEQUENCE CHARACTERISTICS:
54                 (A) LENGTH: 2076 base pairs
55                 (B) TYPE: nucleic acid
56                 (C) STRANDEDNESS: single
57                 (D) TOPOLOGY: linear
58
59             (ii) MOLECULE TYPE: cDNA
60
61             (ix) FEATURE:
62                 (A) NAME/KEY: CDS
63                 (B) LOCATION: 32..1534
64
65             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67   GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA
68       52
69                                        Met Ser Ala Leu Arg Arg Lys
70                                         1               5
71
72   TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC
73   100
74   Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
75           10              15                  20
76
77   TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC
78   148
79   Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
80       25              30                  35
81
82   AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG
83 · 196
84   Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
85    40              45              50                  55
86
87   CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC
88   244
89   Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
90                   60              65                  70
91
92   TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC
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INPUT SET: S32821.raw

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 93   292
 94   Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
 95               75              80                  85
 96
 97   ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG
 98   340
 99   Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
100               90              95                  100
101
102   GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC
103   388
104   Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
105       105             110             115
106
107   TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT        436
108   Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
109   120             125             130             135
110
111   TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC
112   484
113   Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
114               140             145             150
115
116   ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC
117   532
118   Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
119               155             160             165
120
121   CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG
122   580
123   Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
124               170             175             180
125
126   ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT
127   628
128   Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
129       185             190             195
130
131   GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG
132   676
133   Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val
134   200             205             210             215
135
136   GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG
137   724
138   Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys
139               220             225             230
140
141   CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC
142   772
143   Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp
144               235             240             245
145
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146   CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT
147   820
148   Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe
149           250                   255                   260
150
151   CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC
152   868
153   Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro
154           265                   270                   275
155
156   TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG
157   916
158   Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val
159   280                   285                   290                   295
160
161   GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA
162   964
163   Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln
164           300                   305                   310
165
166   GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT
167   1012
168   Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe
169           315                   320                   325
170
171   TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC
172   1060
173   Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser
174           330                   335                   340
175
176   CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA
177   1108
178   Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys
179       345                   350                   355
180
181   GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC
182   1156
183   Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala
184   360                   365                   370                   375
185
186   ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA
187   1204
188   Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly
189               380                   385                   390
190
191   CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG
192   1252
193   Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr
194               395                   400                   405
195
196   GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT
197   1300
198   Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,927*

INPUT SET: S32821.raw

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201   TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA
202   1348
203   Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg
204        425                430                     435
205
206   ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC
207   1396
208   Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr
209   440                445                450                      455
210
211   ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA
212   1444
213   Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro
214                460                 465                  470
215
216   CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT
217   1492
218   Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn
219                475                 480                  485
220
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`-->`
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221   CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA          1534
222   Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
223        490                 495                  500
224
225   TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT
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`-->`
```
226   CCAATATTTG   1594
227
228   GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG
```

`-->`
```
229   GCAAATTCAT   1654
230
231   CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA
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`-->`
```
232   AGGGAGGACA   1714
233
234   TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA
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`-->`
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235   ATGTGCAAAT   1774
236
237   TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA
```

`-->`
```
238   TATTCTGGAA   1834
239
240   AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA
```

`-->`
```
241   ATATATGTAT   1894
242
243   TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG
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`-->`
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244   CATACATACA   1954
245
246   TACATGCATA TGCACAGACA CATACACACA CATACTCATA TATATAAAAC
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`-->`
```
247   ATACCCATAC   2014
248
249   AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA
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`-->`
```
250   AAAAAACTCG   2074
251
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/039,927*

INPUT SET: S32821.raw

252   AG   2076
253
254

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/039,927*

INPUT SET: S32821.raw

Line	Error	Original Text
54	Entered (2076) and Calc. Seq. Length (182) differ	(A) LENGTH: 2076 base pairs
107	# of Sequences for line conflicts w/ running total	TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC
221	# of Sequences for line conflicts w/ running total	CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GA
226	# of Sequences for line conflicts w/ running total	CCAATATTTG 1594
229	# of Sequences for line conflicts w/ running total	GCAAATTCAT 1654
232	# of Sequences for line conflicts w/ running total	AGGGAGGACA 1714
235	# of Sequences for line conflicts w/ running total	ATGTGCAAAT 1774
238	# of Sequences for line conflicts w/ running total	TATTCTGGAA 1834
241	# of Sequences for line conflicts w/ running total	ATATATGTAT 1894
244	# of Sequences for line conflicts w/ running total	CATACATACA 1954
247	# of Sequences for line conflicts w/ running total	ATACCCATAC 2014
250	# of Sequences for line conflicts w/ running total	AAAAAACTCG 2074

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT: Lester, Henry A.
 6                       Davidson, Norman
 7                       Kofuji, Paulo
 8
 9       (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
10              MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
11
12      (iii) NUMBER OF SEQUENCES: 2
13
14       (iv) CORRESPONDENCE ADDRESS:
15              (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
16              (B) STREET: Four Embarcadero Center, Suite 3400
17              (C) CITY: San Francisco
18              (D) STATE: California
19              (E) COUNTRY: United States
20              (F) ZIP: 94111-4187
21
22        (v) COMPUTER READABLE FORM:
23              (A) MEDIUM TYPE: Floppy disk
24              (B) COMPUTER: IBM PC compatible
25              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28       (vi) CURRENT APPLICATION DATA:
29              (A) APPLICATION NUMBER: US 09/039,927
30              (B) FILING DATE: 16-MAR-1998
31              (C) CLASSIFICATION:
32
33      (vii) PRIOR APPLICATION DATA:
34              (A) APPLICATION NUMBER: US 08/066,371
35              (B) FILING DATE: 21-MAR-1993
36
37      (vii) PRIOR APPLICATION DATA:
38              (A) APPLICATION NUMBER: US 08/614,801
39              (B) FILING DATE: 07-MAR-1996
40
41     (viii) ATTORNEY/AGENT INFORMATION:
42              (A) NAME: Trecartin, Richard F.
43              (B) REGISTRATION NUMBER: 31,801
44              (C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
45
46       (ix) TELECOMMUNICATION INFORMATION:
```

```
47              (A) TELEPHONE: (415) 781-1989
48              (B) TELEFAX: (415) 398-3249
49              (C) TELEX: 910 277299
50
51   (2) INFORMATION FOR SEQ ID NO:1:
52
53       (i) SEQUENCE CHARACTERISTICS:
54              (A) LENGTH: 2076 base pairs
55              (B) TYPE: nucleic acid
56              (C) STRANDEDNESS: single
57              (D) TOPOLOGY: linear
58
59      (ii) MOLECULE TYPE: cDNA
60
61      (ix) FEATURE:
62              (A) NAME/KEY: CDS
63              (B) LOCATION: 32..1534
64
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67   GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA     52
68                                     Met Ser Ala Leu Arg Arg Lys
69                                       1                   5
70
71   TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC   100
72   Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
73            10                  15                  20
74
75   TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC   148
76   Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
77        25                  30                  35
78
79   AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG   196
80   Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
81    40                  45                  50                  55
82
83   CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC   244
84   Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
85                60                  65                  70
86
87   TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC   292
88   Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
89                75                  80                  85
90
91   ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG   340
92   Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
93            90                  95                  100
94
95   GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC   388
96   Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
97        105                 110                 115
98
99   TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT   436
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INPUT SET: S32821.raw

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100    Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
101    120                 125                 130             135
102

103    TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC   484
104    Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
105                    140             145             150
106

107    ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC   532
108    Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
109                155                 160             165
110

111    CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG   580
112    Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
113                170                 175             180
114

115    ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT   628
116    Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
117        185                 190             195
118

119    GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG   676
120    Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val
121    200                 205             210                 215
122

123    GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG   724
124    Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys
125                220                 225             230
126

127    CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC   772
128    Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp
129                235                 240             245
130

131    CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT   820
132    Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe
133        250                 255             260
134

135    CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC   868
136    Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro
137        265                 270             275
138

139    TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG   916
140    Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val
141    280                 285             290                 295
142

143    GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA   964
144    Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln
145                300             305                 310
146

147    GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT   1012
148    Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe
149                315             320                 325
150

151    TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC   1060
152    Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser
```

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153            330                    335                    340
154
155   CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA   1108
156   Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys
157        345                    350                    355
158
159   GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC   1156
160   Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala
161   360                    365                    370                    375
162
163   ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA   1204
164   Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly
165                   380                    385                    390
166
167   CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG   1252
168   Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr
169                   395                    400                    405
170
171   GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT   1300
172   Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr
173        410                    415                    420
174
175   TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA   1348
176   Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg
177        425                    430                    435
178
179   ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC   1396
180   Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr
181   440                    445                    450                    455
182
183   ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA   1444
184   Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro
185                   460                    465                    470
186
187   CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT   1492
188   Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn
189                   475                    480                    485
190
191   CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA           1534
192   Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
193                   490                    495                    500
194
195   TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG   1594
196
197   GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT   1654
198
199   CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA   1714
200
201   TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT   1774
202
203   TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA   1834
204
205   AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT   1894
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INPUT SET: S32821.raw

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206
207    TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACATACA    1954
208
209    TACATGCATA TGCACAGACA CATACACACA CATACTCATA TATATAAAAC ATACCCATAC    2014
210
211    AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAACTCG    2074
212
213    AG                                                                  2076
214
215
216    (2) INFORMATION FOR SEQ ID NO:2:
217
218         (i)  SEQUENCE CHARACTERISTICS:
219              (A) LENGTH: 501 amino acids
220              (B) TYPE: amino acid
221              (D) TOPOLOGY: linear
222
223         (ii) MOLECULE TYPE: protein
224
225         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
226
227    Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr
228     1               5                   10                  15
229
230    Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
231                   20                  25                  30
232
233    Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
234               35                  40                  45
235
236    Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
237           50                  55                  60
238
239    Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
240     65                  70                  75                  80
241
242    Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
243                   85                  90                  95
244
245    Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
246                  100                 105                 110
247
248    Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr
249           115                 120                 125
250
251
252    Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile
253           130                 135                 140
254
255    Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile
256    145                 150                 155                 160
257
258    Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
```

****** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

```
51    (2) INFORMATION FOR SEQ ID NO:1:
52
53        (i) SEQUENCE CHARACTERISTICS:
54            (A) LENGTH: 2076 base pairs
55            (B) TYPE: nucleic acid
56            (C) STRANDEDNESS: single
57            (D) TOPOLOGY: linear
58
59       (ii) MOLECULE TYPE: cDNA
60
61       (ix) FEATURE:
62            (A) NAME/KEY: CDS
63            (B) LOCATION: 32..1534
64
65       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67   GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA      52
68                                     Met Ser Ala Leu Arg Arg Lys
69                                      1                   5
70
71   TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC    100
72   Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
73          10                  15                  20
74
75   TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC    148
76   Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
77       25                  30                  35
78
79   AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG    196
80   Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
81    40                  45                  50                  55
82
83   CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC    244
84   Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
85                  60                  65                  70
86
87   TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC    292
.88  Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
89                  75                  80                  85
90
91   ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG    340
92   Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
93              90                  95                  100
94
95   GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC    388
96   Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
97       105                 110                 115
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 98
 99    TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT   436
100    Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
101    120                 125                 130                 135
102
103    TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC   484
104    Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
105                        140                 145                 150
106
107    ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC   532
108    Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
109                    155                 160                 165
110
111    CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG   580
112    Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
113                170                 175                 180
114
115    ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT   628
116    Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
117        185                 190                 195
118
119    GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG   676
120    Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val
121    200                 205                 210                 215
122
123    GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG   724
124    Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys
125                    220                 225                 230
126
127    CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC   772
128    Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp
129                235                 240                 245
130
131    CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT   820
132    Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe
133                250                 255                 260
134
135    CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC   868
136    Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro
137        265                 270                 275
138
139    TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG   916
140    Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val
141    280                 285                 290                 295
142
143    GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA   964
144    Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln
145                    300                 305                 310
146
147    GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT  1012
148    Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe
149                315                 320                 325
150
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INPUT SET: S32821.raw

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151  TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC  1060
152  Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser
153          330                 335                 340
154
155  CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA  1108
156  Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys
157          345                 350                 355
158
159  GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC  1156
160  Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala
161  360                 365                 370                 375
162
163  ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA  1204
164  Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly
165              380                 385                 390
166
167  CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG  1252
168  Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr
169              395                 400                 405
170
171  GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT  1300
172  Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr
173          410                 415                 420
174
175  TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA  1348
176  Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg
177          425                 430                 435
178
179  ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC  1396
180  Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr
181  440                 445                 450                 455
182
183  ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA  1444
184  Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro
185              460                 465                 470
186
187  CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT  1492
188  Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn
189              475                 480                 485
190
191  CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA          1534
192  Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
193          490                 495                 500
194
195  TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG  1594
196
197  GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT  1654
198
199  CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA  1714
200
201  TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT  1774
202
203  TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA  1834
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/039,927*

INPUT SET: S32821.raw

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204
205    AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT    1894
206
207    TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACATACA    1954
208
209    TACATGCATA TGCACAGACA CATACACACA CATACTCATA TATATAAAAC ATACCCATAC    2014
210
211    AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAACTCG    2074
212
213    AG                                                                  2076
214
215
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/039,927*

INPUT SET: S32821.raw

Line	Error	Original Text